

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 21, 2002, 10:15:23 ; Search time 30.33 Seconds  
(without alignments)  
1102.315 Million cell updates/sec

Title: US-09-758-017A-2  
Perfect score: 1603  
Sequence: 1 MLFKLGICQRCISSNRVLPG.....SKANGLLKLSGTEPINRRL 301

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_032802:\*  
1: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.\*  
2: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.\*  
3: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.\*  
4: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.\*  
5: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT.\*  
6: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT.\*  
7: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT.\*  
8: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT.\*  
9: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT.\*  
10: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT.\*  
11: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT.\*  
12: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT.\*  
13: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT.\*  
14: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT.\*  
15: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT.\*  
16: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT.\*  
17: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT.\*  
18: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT.\*  
19: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.\*  
20: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.\*  
21: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.\*  
22: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1596	99.6	301	AAU04939	Atlantic cod heat-
2	1421	88.6	301	AAU04940	Atlantic cod heat-
3	1030.5	64.3	292	AAAG74939	Human colon cancer
4	1018.5	63.5	313	AAW21814	Uracil DNA glycosy
5	1015.5	63.3	313	AAW21823	Mutant uracil DNA
6	1014.5	63.3	313	AAW21822	Mutant uracil DNA
7	1014.5	63.3	313	AAW21820	Mutant uracil DNA
8	1013.5	63.2	313	AAW21821	Mutant uracil DNA
9	1013.5	63.2	313	AAW21815	Cytosine DNA glyco
10	1012.5	63.2	313	AAW21824	Mutant uracil DNA
11	1011.5	63.1	313	AAW21819	Mutant uracil DNA

12	1009.5	63.0	313	18	AAW21816	Thymine DNA glycos
13	1007.5	62.9	313	18	AAW21825	Mutant uracil DNA
14	681.5	42.5	229	22	AAU069754	Escherichia coli u
15	635.5	39.6	219	22	AAAB8498	Haemophilus influe
16	598.5	37.3	321	21	AAAG14409	Arabidopsis thalia
17	598.5	37.3	320	21	AAAG14408	Arabidopsis thalia
18	591.5	36.9	227	20	AAU01335	B. pallidus uracil
19	539.5	33.7	236	20	AAAY35405	Chlamydia pneumoni
20	539	33.6	229	20	AAAY37595	Amino acid sequenc
21	520	32.4	216	22	AAAG81666	S. epidermidis ope
22	444.5	27.7	255	21	AAAB53166	Macaca mulatta rha
23	423	26.4	334	19	AAW72171	HSV-2 strain SB5 C
24	423	26.4	334	19	AAW72090	HSV-2 strain SB5 C
25	423	26.4	334	19	AAW72005	HSV-2 strain SB5 C
26	415	25.9	293	19	AAW80437	Feline herpesvirus
27	384	24.0	233	19	AAAG98728	H. pylori GHPO 902
28	366.5	22.9	254	22	AAAG1207	C. glutamicum prote
29	345	21.5	264	22	AAU55037	Propionibacterium
30	303	18.9	995	22	ABG11717	Novel human diagno
31	275	17.2	72	21	AAAB4117	Human cancer assoc
32	125	7.8	29	20	AAAY42895	Human wild-type ur
33	116	7.2	29	20	AAAY50001	Human mutant uraci
34	112	7.0	29	20	AAAY50002	Human mutant uraci
35	104	6.5	1069	22	ABAB63364	Drosophila melanog
36	90.5	5.6	506	22	ABB72057	Drosophila melanog
37	89.5	5.6	931	22	AAAM39815	Human polypeptide
38	89	5.6	752	15	AAAS1701	AML1-MFG8 fusion.
39	87.5	5.5	1005	22	ABG11447	Novel human diagno
40	87	5.4	1362	22	AAU38416	Salmonella typhi c
41	86	5.4	498	21	AAAB13559	Streptomyces globi
42	84.5	5.3	797	17	AAW05290	Triticum tauschii
43	84.5	5.3	2271	22	ABB65616	Drosophila melanog
44	83	5.2	29	20	AAAY42896	Yeast uracil DNA g
45	82.5	5.1	547	10	AAAP94045	t-plastin derived

ALIGNMENTS

RESULT 1  
AAU04939  
ID AAU04939 standard; Protein; 301 AA.  
XX  
AC AAU04939;  
XX  
DT 24-OCT-2001 (first entry)  
XX  
DE Atlantic cod heat-labile uracil-DNA glycosylase, UNG #1.  
XX  
KW Atlantic cod; heat-labile uracil-DNA glycosylase; UNG; UDG;  
KW PCR control; LCR control; ligase chain reaction; carry-over prevention.  
XX  
OS Gadus morhua.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 17 /note= "Encoded by GTY"  
FT  
XX  
PN WO200151623-A1.  
XX  
PD 19-JUL-2001.  
XX  
PF 10-JAN-2001; 2001WO-N000008.  
XX  
PR 12-JAN-2000; 2000NO-0000163.  
PR 27-OCT-2000; 2000NO-0005428.  
XX  
PA (BIOT-) BIOTEC ASA.  
XX  
PI Lanes O, Willasen NP, Guddal PH, Gjellesvik DR;  
XX  
DR WPI: 2001-451854/48.  
DR N-PSDB; AAS09498.

```

XX New cod liver uracil-DNA glycosylase enzyme, useful in monitoring or
PT controlling a reaction system multiplying DNA sequences or in
PT carry-over prevention procedures -
XX
XX Claim 2; Page 52-54; 59pp; English.
XX
CC The sequence is an Atlantic cod heat-labile uracil-DNA glycosylase,
CC (UNG/UDG). The enzyme is useful in monitoring and/or controlling a
CC reaction system multiplying DNA sequences, e.g. PCR (polymerase chain
CC reaction) or LCR (ligase chain reaction). The enzyme is also useful in
CC carry-over prevention procedures.
XX
XX Sequence 301 AA;
SQ
    Query Match          99.6%; Score 1596; DB 22; Length 301;
    Best Local Similarity 99.7%; Pred. No. 9e-156;
    Matches 300; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MLFKGLGQCRCISSNRVLPGLLIPOTLCFSKLMKIPPKLRSSNVBQKTSPPQLSVEQLE 60
DB 1 mlfkglcqcrcissnrvlpgllipqtlcfsklmktpkklrsvnveqktsppqlsveqle 60
QY 61 RMAKNKKAALDKIRAKATPAGFETWRRELAAEFKPYFKQLMSFVADERSRHTVYPPAD 120
DB 1 rmaknkkaaldkirakatpagfetwrrelaaefekpyfkqlmsfvadersrhtvypad 120
QY 121 QVYSSTEMCDIODVKVILGQDPYHCPNQAHLGCLFSVQKPPPPPSLVNIYKELCTDIDG 180
DB 121 qvysstemcdiodvkvilgqdpynghqahglcfsvqkpppppslvniykelctdidg 180
QY 181 FKHPGHGDLGSAKOGVLLNNAVLTVRAHQANSHKDRGWETFTDAVIKWSNREGVWFL 240
DB 181 fkhpghdlsgakogvlllnnavltvraqanshkdrgwetftdavikwslvnregvfl 240
QY 241 LMGSAHKKGATIDKRHHVLAQVHPSPLSAHRGFLGCKHFSKANGLLKLSGTEPINWRA 300
DB 241 lmgayahkkgatidkrhhvlgavhpsplsahrgflgckhfskangllklsgtepinwra 300
QY 301 L 301
DB 301 L 301

RESULT 2
AAU04940
ID AAU04940 standard; Protein; 301 AA.
XX
AC AAU04940;
XX
DT 24-OCT-2001 (first entry)
XX
DE Atlantic cod heat-labile uracil-DNA glycosylase, UNG #2.
XX
DE Atlantic cod; heat-labile uracil-DNA glycosylase; UNG; UDG;
KW PCR control; LCR control; ligase chain reaction; carry-over prevention.
XX
OS Gadus morhua.
XX
XX WO200151623-A1.
PN
XX 19-JUL-2001.
PD
XX 10-JAN-2001; 2001WO-NO00008.
PF
XX 12-JAN-2000; 2000NO-0000163.
PR
XX 27-OCT-2000; 2000NO-0005428.
XX
PA (BIOT-) BIOTEC ASA.
XX
PI Lanes O, Willasen NP, Guddal PH, Gjellesvik DR;
DR

```

```

DR WPI; 2001-451854/48.
DR N-PSDB; AAS09499.
XX
XX New cod liver uracil-DNA glycosylase enzyme, useful in monitoring or
PT controlling a reaction system multiplying DNA sequences or in
PT carry-over prevention procedures -
XX
XX Claim 2; Page 54-56; 59pp; English.
XX
CC The sequence is an Atlantic cod heat-labile uracil-DNA glycosylase,
CC (UNG/UDG). The enzyme is useful in monitoring and/or controlling a
CC reaction system multiplying DNA sequences, e.g. PCR (polymerase chain
CC reaction) or LCR (ligase chain reaction). The enzyme is also useful in
CC carry-over prevention procedures.
XX
XX Sequence 301 AA;
SQ
    Query Match          88.6%; Score 1421; DB 22; Length 301;
    Best Local Similarity 98.9%; Pred. No. 9.4e-138;
    Matches 266; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 33 MKITPKLLSSNVBQKTSPPQLSVEQLERMAKNKKAALDKIRAKATPAGFETWRRELAA 92
DB 33 vqitpkllrsvnveqktsppqlsveqlermaknkkaaldkirakatpagfetwrrelaa 92
QY 93 EFEKPYFKQLMSFVADERSRHTVYPPADOVYSTEMCDIODVKVILGQDPYHCPNQAHG 152
DB 93 efekpyfkqlmsfvadersrhtvypadqyvwtemcdiodkvkvlvgdpyhgpqhahg 152
QY 153 LCFSVQKPPPPPSLVNIYKELCTDIDGPKHPGHGDLGSAKOGVLLNNAVLTVRAHQAN 212
DB 153 lcfsvqkpppppslvniykelctdidgfkphghdlsgakogvlllnnavltvraqan 212
QY 213 SHKDRGWETFTDAVIKWSNREGVWFLWGSYAHKKGATIDKRHHVLAQVHPSPLSAH 272
DB 213 shkdrgetftdavikwslvnregvflwgsyahkkgatidkrhhvlgavhpsplsah 272
QY 273 RGFLGCKHFSKANGLLKLSGTEPINWRA 301
DB 273 rgflgckhfskangllklsgtepinwral 301

RESULT 3
AAG74939
ID AAG74939 standard; Protein; 292 AA.
XX
AC AAG74939;
XX
DT 03-SEP-2001 (first entry)
XX
DE Human colon cancer antigen protein SEQ ID NO:5703.
XX
DE Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW colorectal carcinoma; chromosome 12.
XX
OS Homo sapiens.
XX
XX WO200122920-A2.
PN
XX 05-APR-2001.
PD
XX 28-SEP-2000; 2000WO-US26524.
PF
XX 29-SEP-1999; 99US-0157137.
PR 03-NOV-1999; 99US-0163280.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX Ruben SM, Barash SC, Birse CE, Rosen CA;
PI
XX WPI; 2001-235357/24.
DR N-PSDB; AAH34344.
DR

```



```
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Misc-difference 178
XX FT /note= "site of Ser-178 to Ala substn."
XX XX WO9725416-A2.
XX PD 17-JUL-1997.
XX PE 09-JAN-1997; 97WO-GB000057.
XX PR 09-JAN-1996; 96GB-0000384.
XX XX (DZIE/) DZIEGLEWSKA H E.
XX PA (NYFO-) NYFOTEK AS.
XX PI Kavli B, Krokan HE, Mol CD, Slupphaug G, Tainer JA;
XX DR WPI; 1997-372857/34.
XX XX DNA glycosylase capable of releasing cytosine, thymine or uracil
XX PT bases from DNA - useful in vitro and/or vivo mutagenesis systems
XX PT to remove contaminating DNA prior to PCR amplification
XX PS Example 3; Refer to Page 47-48; 60pp; English.
XX XX Mutant DNA glycosylases (AAW21819-256) were produced by site-directed
XX CC mutagenesis of human uracil DNA glycosylase UNG2 cDNA (see also
XX CC AAT73564) and expression in Escherichia coli. None of these mutants
XX CC showed cytosine DNA glycosylase or thymine DNA glycosylase
XX CC activity. In contrast, an N204D substn. (see also AAW21815)
XX CC provided cytokine DNA glycosylase activity, and a Y147A substn.
XX CC (see also AAW21816) provided thymine DNA glycosylase activity. The
XX CC results demonstrated the significance of Asn204 for specific
XX CC binding of uracil-containing DNA and the significance of the Tyr147
XX CC side chain ring structure for preventing binding of thymine.
XX SQ Sequence 313 AA;
Query Match 63.3%; Score 1015.5; DB 18; Length 313;
Best Local Similarity 69.5%; Pred. No. 5.7e-96;
Matches 187; Conservative 32; Mismatches 47; Indels 3; Gaps 2;
QY 35 ITPKKLRSSNVEQKT--SSPOLSVQEQLERMAKNKKAALDKIRAKATPAGFGETWRRELA 92
Db 46 lpakkapaggeqptppssp-lsaeqldirgnkaaalrlaarnvpgfgeswkkhlsq 104
QY 93 EFEKPYFKQLMSFVADERSRHTVPPADQVYSSTEMCDIQDKVVIILGQDPYHGPNQAHG 152
Db 105 efgkpyfiklmgfvaerkyhtvppphqyftwtqmcddkdvkvilgqdpfghpncqahg 164
QY 153 LCFSVQKVPVPPPSLVNIYKELCTDIDGFKHPGHGDLGSAKOGVLLNNAVLTVRAHQAN 212
Db 165 lcfsvqrpvpppsalenlykelstdiedfwhpgdglsgwakgqgvlllnnavltvrahan 224
QY 213 SHKDRGWETFTDAVWKVLSVNRGVEFLLMGSAHKKGATIDRKRHHVLQAVHPSPLSAH 272
Db 225 shkerqweqftdavvwnqnsnglvllwgsyaqkgsaidrkrhvlqtahpsplsvy 284
QY 273 RGFGLGCKHFSKANGLLKLSGTEPINWRAL 301
Db 285 rgffgcrhfsktnellqksgkpidwkel 313
RESULT 6
AAW21822
ID AAW21822 standard; Protein; 313 AA.
XX AC
XX AAW21822;
XX XX
```

```
DT 28-SEP-1997 (first entry)
XX DE Mutant uracil DNA glycosylase (Y147F).
XX XX Uracil DNA glycosylase; UNG2; mutagenesis.
XX KW Synthetic.
XX OS Key Location/Qualifiers
XX FH Misc-difference 156 /note= "site of Tyr-147 to Phe substn."
XX FT WO9725416-A2.
XX PN 17-JUL-1997.
XX PD 09-JAN-1997; 97WO-GB000057.
XX PF 09-JAN-1996; 96GB-0000384.
XX PR (DZIE/) DZIEGLEWSKA H E.
XX PA (NYFO-) NYFOTEK AS.
XX PI Kavli B, Krokan HE, Mol CD, Slupphaug G, Tainer JA;
XX DR WPI; 1997-372857/34.
XX XX DNA glycosylase capable of releasing cytosine, thymine or uracil
XX PT bases from DNA - useful in vitro and/or vivo mutagenesis systems
XX PT to remove contaminating DNA prior to PCR amplification
XX PS Example 3; Refer to Page 47-48; 60pp; English.
XX XX Mutant DNA glycosylases (AAW21819-256) were produced by site-directed
XX CC mutagenesis of human uracil DNA glycosylase UNG2 cDNA (see also
XX CC AAT73564) and expression in Escherichia coli. None of these mutants
XX CC showed cytosine DNA glycosylase or thymine DNA glycosylase
XX CC activity. In contrast, an N204D substn. (see also AAW21815)
XX CC provided cytokine DNA glycosylase activity, and a Y147A substn.
XX CC (see also AAW21816) provided thymine DNA glycosylase activity. The
XX CC results demonstrated the significance of Asn204 for specific
XX CC binding of uracil-containing DNA and the significance of the Tyr147
XX CC side chain ring structure for preventing binding of thymine.
XX SQ Sequence 313 AA;
```

```
Query Match 63.3%; Score 1014.5; DB 18; Length 313;
Best Local Similarity 69.5%; Pred. No. 7.2e-96;
Matches 187; Conservative 32; Mismatches 47; Indels 3; Gaps 2;
QY 35 ITPKKLRSSNVEQKT--SSPOLSVQEQLERMAKNKKAALDKIRAKATPAGFGETWRRELA 92
Db 46 lpakkapaggeqptppssp-lsaeqldirgnkaaalrlaarnvpgfgeswkkhlsq 104
QY 93 EFEKPYFKQLMSFVADERSRHTVPPADQVYSSTEMCDIQDKVVIILGQDPYHGPNQAHG 152
Db 105 efgkpyfiklmgfvaerkyhtvppphqyftwtqmcddkdvkvilgqdpfghpncqahg 164
QY 153 LCFSVQKVPVPPPSLVNIYKELCTDIDGFKHPGHGDLGSAKOGVLLNNAVLTVRAHQAN 212
Db 165 lcfsvqrpvpppsalenlykelstdiedfwhpgdglsgwakgqgvlllnnavltvrahan 224
QY 213 SHKDRGWETFTDAVWKVLSVNRGVEFLLMGSAHKKGATIDRKRHHVLQAVHPSPLSAH 272
Db 225 shkerqweqftdavvwnqnsnglvllwgsyaqkgsaidrkrhvlqtahpsplsvy 284
QY 273 RGFGLGCKHFSKANGLLKLSGTEPINWRAL 301
Db 285 rgffgcrhfsktnellqksgkpidwkel 313
```

RESULT 7



160	efgkpyfiklmgfvaerkyhvyppphqvftrqcmcdikdvkvlllgdqpyhpnqahg	216
Db		
105	LCFSVQKVPVPPPPSLVNIIYKELCETDIDGFKHPHGDLGSNAKQGVLLNLAVLTVRAHQAN	212
Qy		
153	LCFSVQKVPVPPPPSLVNIIYKELCETDIDGFKHPHGDLGSNAKQGVLLNLAVLTVRAHQAN	212
Qy		
165	LCFSVQKVPVPPPPSLVNIIYKELCETDIDGFKHPHGDLGSNAKQGVLLNLAVLTVRAHQAN	212
Db		
213	SHKDRGWETFDVAVIKWLSVNRQGVVFLLMGSAHYAKKGAITIDRKRHHVLQAVHPSPLSAH	272
Qy		
225	SHKDRGWETFDVAVIKWLSVNRQGVVFLLMGSAHYAKKGAITIDRKRHHVLQAVHPSPLSAH	272
Qy		
275	SHKDRGWETFDVAVIKWLSVNRQGVVFLLMGSAHYAKKGAITIDRKRHHVLQAVHPSPLSAH	272
Qy		
285	SHKDRGWETFDVAVIKWLSVNRQGVVFLLMGSAHYAKKGAITIDRKRHHVLQAVHPSPLSAH	272
Qy		

QY	273	RGFLGCKHFHSKANGLLKLSGTPEPINWRAL	301
Db	285	raffacrfhskstnelaksgakpoidwkel	313

DE	Mutant uracil DNA glycosylase (N204Q).
XX	
XX	
KW	Uracil DNA glycosylase; UNG2; mutagenesis.
XX	
XX	
OS	Synthetic.
XX	
XX	
FH	Key
FH	Location/Qualifiers
FT	Misc-difference 213
FT	/note= "site of Asn-213 to Gln substn."
FT	

Example 3: Refer to Page 47-48; 60pp; English.

Mutant DNA glycosylases (AAW21819-256) were produced by site-directed mutagenesis of human uracil DNA glycosylase UNG2 cDNA (see also AAW73564) and expression in *Escherichia coli*. None of these mutants showed cytosine DNA glycosylase or thymine DNA glycosylase activity. In contrast, an N204D substn. (see also AAW21815) provided cytosine DNA glycosylase activity, and a Y147A substn. (see also AAW21816) provided thymine DNA glycosylase activity. The results demonstrated the significance of Asn204 for specific binding of uracil-containing DNA and the significance of the Tyr147 side chain ring structure for preventing binding of thymine.

CC	provided cytokine DNA glycosylase activity, and a Y147A substn.
CC	(see also AaW21816) provided thymine DNA glycosylase activity. The
CC	results demonstrated the significance of Asn204 for specific
CC	binding of uracil-containing DNA and the significance of the Tyr147
CC	side chain ring structure for preventing binding of thymine.
XX	Sequence 313 AA;

Query Match 63.2%; Score 1012.5; DB 18; Length 313;  
Best Local Similarity 69.5%; Pred. No. 1.2e-95;  
Matches 187; Conservative 31; Mismatches 48; Indels 3; Gaps  
QY 35 ITPKKLRSSNVEQKT--SSPOLSVQLERMAKNKAALDKIRAKATPAGFGETWRRELA 92

```

Query_Match      63.2%; Score 1012.5; DB 18; Length 313;
Best Local Similarity 69.5%; Pred. No. 1.2e-95;
Matches 187; Conservative 31; Mismatches 48; Indels 3; Gaps 2
QV      35 ITPKLRSSNVBQKTL--SSPQLSVLEQLERMAKNKKAALDKIRAKATPAFGFTWRRELA 92

```

Db 46 ipakkapaggepgtpssp-lsaeqlidriqrnkaaallrlaarnvpgfgeswkkhls 104

QY 93 EFEKPYFKQLMSFVADERSRHTVYPPADQVYSTEMCDIODVKVILGQDPYHGPNOAHG 152

Db 105 efdgkpyfikimgfvaeeerkhytvyppphqyftwtqmcidkdvkvilgqdpvhgpnqahg 164

QY 153 LCFSVOKPVPVPPPSLVNIVKELCTDIDGFKHPGHGDLGSGWAKOGVLLLNVLTVRAHQAN 212

Db 165 lcfsvqrpvpppsleniykelstiedfvpghngdlsqwakgvglllqavltvranqan 224

QY 213 SHKDRGWETFDVIRKWSYNREGVFLLMGSAHKKGATIDRKRHHVLAQVHPSPLSAH 272

Db 225 shkergweqftdavswnqnsnglvfllwgsyaqkgsaidrkrhhvltqahpsplsly 284

QY 273 RGFLGCKHFSKANGLLKLSGTEPINWRAL 301

Db 285 rgfgrhfsktnellqsgkkipdwkel 313

RESULT 11

AAW21819

ID AAW21819 standard; Protein; 313 AA.

AC AAW21819;

DT 28-SEP-1997 (first entry)

XX Mutant uracil DNA glycosylase (Q144L).

XX Uracil DNA glycosylase; UNG2; mutagenesis.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 153

FT /note= "site of Gln-144 to Leu substn."

XX WO9725416-A2.

XX 17-JUL-1997.

XX 09-JAN-1997; 97WO-GB000057.

XX 09-JAN-1996; 96GB-0000384.

XX (DZIE/) DZIEGLEWSKA H E.

XX (NYFO-) NYFOTEK AS.

XX Kavli B, Krokan HE, Mol CD, Slupphaug G, Tainer JA;

XX WPI; 1997-372857/34.

XX DNA glycosylase capable of releasing cytosine, thymine or uracil

PT bases from DNA - useful in vitro and/or vivo mutagenesis systems

PT to remove contaminating DNA prior to PCR amplification

PS Example 3; Refer to Page 47-48; 60pp; English.

XX Mutant DNA glycosylases (AAW21819-256) were produced by site-directed

CC mutagenesis of human uracil DNA glycosylase UNG2 cDNA (see also

CC AAT73564) and expression in Escherichia coli. None of these mutants

CC showed cytosine DNA glycosylase or thymine DNA glycosylase

CC activity. In contrast, an N204D substn. (see also AAW21815)

CC provided cytosine DNA glycosylase activity, and a Y147A substn.

CC (see also AAW21816) provided thymine DNA glycosylase activity. The

CC results demonstrated the significance of Asn204 for specific

CC binding of uracil-containing DNA and the significance of the Tyr147

CC side chain ring structure for preventing binding of thymine.

XX Sequence 313 AA;

Query Match 63.1%; Score 1011.5; DB 18; Length 313;

Best Local Similarity 69.5%; Pred. No. 1.5e-95;

Matches 187; Conservative 31; Mismatches 48; Indels 3; Gaps 2;

QY 35 ITPKKLRSSNVEQKT--SSPOLSVQEQLERMAKNKKAALDKIRAKATPAGFGETWRRELA 92

Db 46 ipakkapaggepgtpssp-lsaeqlidriqrnkaaallrlaarnvpgfgeswkkhls 104

QY 93 EFEKPYFKQLMSFVADERSRHTVYPPADQVYSTEMCDIODVKVILGQDPYHGPNOAHG 152

Db 105 efdgkpyfikimgfvaeeerkhytvyppphqyftwtqmcidkdvkvilgqdpvhgpnqahg 164

QY 153 LCFSVOKPVPVPPPSLVNIVKELCTDIDGFKHPGHGDLGSGWAKOGVLLLNVLTVRAHQAN 212

Db 165 lcfsvqrpvpppsleniykelstiedfvpghngdlsqwakgvglllqavltvranqan 224

QY 213 SHKDRGWETFDVIRKWSYNREGVFLLMGSAHKKGATIDRKRHHVLAQVHPSPLSAH 272

Db 225 shkergweqftdavswnqnsnglvfllwgsyaqkgsaidrkrhhvltqahpsplsly 284

QY 273 RGFLGCKHFSKANGLLKLSGTEPINWRAL 301

Db 285 rgfgrhfsktnellqsgkkipdwkel 313

RESULT 12

AAW21816

ID AAW21816 standard; Protein; 313 AA.

AC AAW21816;

DT 28-SEP-1997 (first entry)

XX Thymine DNA glycosylase.

XX Thymine DNA glycosylase; uracil DNA glycosylase; UNG2; mutagenesis;

XX DNA sequencing; DNA modification; cell killing.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 156

FT /note= "site of Tyr-147 to Ala substn."

XX WO9725416-A2.

XX 17-JUL-1997.

XX 09-JAN-1997; 97WO-GB000057.

XX 09-JAN-1996; 96GB-0000384.

XX (DZIE/) DZIEGLEWSKA H E.

XX (NYFO-) NYFOTEK AS.

XX Kavli B, Krokan HE, Mol CD, Slupphaug G, Tainer JA;

XX WPI; 1997-372857/34.

XX DNA glycosylase capable of releasing cytosine, thymine or uracil

PT bases from DNA - useful in vitro and/or vivo mutagenesis systems

PT to remove contaminating DNA prior to PCR amplification

XX Claim 13; Refer to page 47-48; 60pp; English.

XX A novel thymine DNA glycosylase (TDG) (AAW21816) is capable of

CC releasing both thymine and uracil bases from single and/or double

CC stranded DNA. It is obtd. by site-directed mutagenesis of human

CC uracil DNA glycosylase UNG2 cDNA (see also AAT73564) such that the

CC encoded polypeptide has a Tyr-147 to Ala amino acid substn. that

CC results in gain of TDG activity. Recombinant enzyme can be

CC expressed in transformed host cells for use in mutagenesis (in

CC vivo or in vitro) systems, to remove contaminating DNA prior to

CC PCR, in DNA modification, in cell killing, and in DNA sequencing  
 CC to determine the position of cytokine bases.  
 XX  
 SQ Sequence 313 AA;  
 Query Match 63.0%; Score 1009.5; DB 18; Length 313;  
 Best Local Similarity 69.5%; Pred. No. 2.3e-95;  
 Matches 187; Conservative 31; Mismatches 48; Indels 3; Gaps 2;  
 QY 35 ITPFKLRSSNVEQKT--SSPQLSVEQLERMAKNKKAALDKIRAKATPAGFGETWRRELA 92  
 Db 46 Ipkkapagaggeptppssp-lsaeqldriqrkaaalrlaarnvpgfgeswkkhlsq 104  
 QY 93 EFEKPYFKOLMSFVADERSRHTVPPADQVYSTCMCIQDVKVVILGQDPYHGPNQAHG 152  
 Db 105 efkqpyfiklmfvaeerkytvyppphqvftwtqmcidkdvkvilgqdpahgpnqahq 164  
 QY 153 LCFSVQKVPVPPPSLNVNIYKELCTDIDGFKHPGHGDLGSGWAKOGVLLNNAVLTVRAHQAN 212  
 Db 165 lcfsvqrpvpvpppsleniykelstidiedfvhpgdglsgwakgvlllnavltvrahqan 224  
 QY 213 SHKDRGWETFTDAVIKWLNVNREGVVLWGSVAHKKGATIDRKRHHVLAQVHPSPLSAH 272  
 Db 225 shkerqeqtdavsvlnqnsnglvllwgsyaqkksaidrkrhviqtahpsplsvy 284  
 QY 273 RGFGLGCKHFSGKANGLLKLSGTEPINNRAL 301  
 Db 285 rgfgrhfsktnellqsgkkipdwkel 313  
 RESULT 13  
 AAW21825  
 ID AAW21825 standard; Protein; 313 AA.  
 XX  
 AC AAW21825;  
 XX  
 DT 28-SEP-1997 (first entry)  
 DE  
 DE Mutant uracil DNA glycosylase (H268L).  
 KW Uracil DNA glycosylase; UNG2; mutagenesis.  
 XX  
 OS Synthetic.  
 FH Key Location/Qualifiers  
 FT Misc-difference 277 /note= "site of His-277 to Leu substn."  
 FT  
 XX  
 PN W09725416-A2.  
 XX  
 PD 17-JUL-1997.  
 XX  
 PF 09-JAN-1997; 97WO-CB00057.  
 XX  
 PR 09-JAN-1996; 96GB-0000384.  
 XX  
 PA (DZIE/) DZIEGLEWSKA H E.  
 PA (NYFO-) NYFOTEK AS.  
 XX  
 PI Kavli B, Krokan HE, Mol CD, Slupphaug G, Tainer JA;  
 XX  
 DR WPI; 1997-372857/34.  
 XX  
 PT DNA glycosylase capable of releasing cytosine, thymine or uracil  
 PT bases from DNA - useful in vitro and/or vivo mutagenesis systems  
 PT to remove contaminating DNA prior to PCR amplification  
 XX  
 PS Example 3; Refer to Page 47-48; 60pp; English.  
 XX  
 CC Mutant DNA glycosylases (AAW21819-256) were produced by site-directed  
 CC mutagenesis of human uracil DNA glycosylase UNG2 cDNA (see also  
 CC AAW73564) and expression in Escherichia coli. None of these mutants

CC showed cytosine DNA glycosylase or thymine DNA glycosylase  
 CC activity. In contrast, an N204D substn. (see also AAW21815)  
 CC provided cytokine DNA glycosylase activity, and a Y147A substn. The  
 CC (see also AAW21816) provided thymine DNA glycosylase activity. The  
 CC results demonstrated the significance of Asn204 for specific  
 CC binding of uracil-containing DNA and the significance of the Tyr147  
 CC side chain ring structure for preventing binding of thymine.  
 XX  
 SQ Sequence 313 AA;  
 Query Match 62.9%; Score 1007.5; DB 18; Length 313;  
 Best Local Similarity 69.5%; Pred. No. 3.8e-95;  
 Matches 187; Conservative 31; Mismatches 48; Indels 3; Gaps 2;  
 QY 35 ITPFKLRSSNVEQKT--SSPQLSVEQLERMAKNKKAALDKIRAKATPAGFGETWRRELA 92  
 Db 46 Ipkkapagaggeptppssp-lsaeqldriqrkaaalrlaarnvpgfgeswkkhlsq 104  
 QY 93 EFEKPYFKOLMSFVADERSRHTVPPADQVYSTCMCIQDVKVVILGQDPYHGPNQAHG 152  
 Db 105 efkqpyfiklmfvaeerkytvyppphqvftwtqmcidkdvkvilgqdpahgpnqahq 164  
 QY 153 LCFSVQKVPVPPPSLNVNIYKELCTDIDGFKHPGHGDLGSGWAKOGVLLNNAVLTVRAHQAN 212  
 Db 165 lcfsvqrpvpvpppsleniykelstidiedfvhpgdglsgwakgvlllnavltvrahqan 224  
 QY 213 SHKDRGWETFTDAVIKWLNVNREGVVLWGSVAHKKGATIDRKRHHVLAQVHPSPLSAH 272  
 Db 225 shkerqeqtdavsvlnqnsnglvllwgsyaqkksaidrkrhviqtahpsplsvy 284  
 QY 273 RGFGLGCKHFSGKANGLLKLSGTEPINNRAL 301  
 Db 285 rgfgrhfsktnellqsgkkipdwkel 313  
 RESULT 14  
 AAW69754  
 ID AAW69754 standard; Protein; 229 AA.  
 XX  
 AC AAW69754;  
 XX  
 DT 29-JAN-2002 (first entry)  
 DE  
 DE Escherichia coli uracil DNA glycosylase (ung) polypeptide.  
 KW DNA mutation-binding protein; nuclease; DNA mismatch; cancer;  
 KW DNA damage; human xeroderma pigmentosum complementation group; XPF; XPA;  
 KW XPC; XPE; ERCC4; human Muts homolog 2; hMSH2; Muts; Nuc; MutY; Fpg;  
 KW Fapy-DNA glycosylase; uracil DNA glycosylase; ung; TDG; xtha gene; Uvr A;  
 KW A/G-specific adenine glycosylase; synthetic T4 endonuclease V; T4 endo V;  
 KW thymine DNA-glycosylase; Uvr B; Uvr C; nth gene; nfo gene; exonuclease;  
 KW endonuclease.  
 XX  
 OS Escherichia coli.  
 XX  
 PN W0200173079-A2.  
 XX  
 PD 04-OCT-2001.  
 XX  
 PF 26-MAR-2001; 2001WO-US09700.  
 XX  
 PR 28-MAR-2000; 2000US-192764P.  
 PR 29-AUG-2000; 2000US-0650855.  
 XX  
 PA (REGC ) UNIV CALIFORNIA.  
 XX  
 PI Mc Cutchen-maloney SL;  
 XX  
 DR WPI; 2001-656920/75.  
 DR N-PSDB; AAS63241.  
 XX  
 PT Recombinant chimeric protein, useful for detecting and quantifying DNA





